

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 9, 2006, 13:09:16 / Search time 50 Seconds
(without alignments)
9.921 Million cell updates/sec

Title: US-10-705-857-2
Perfect score: 30
Sequence: 1 MEMQR 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

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Prod. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived from analysis of the total score distribution.

SUMMARIES

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7	30	100.0	206	2	US-08-819-286-1
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OM protein - protein search, using sw model

Run on: February 9, 2006, 13:13:17 / Search time 63 Seconds
(without alignments)
39.793 Million cell updates/sec

Title: US-10-705-857-2

Perfect score: 30
Sequence: 1 BEMQRR 6

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 1000 summaries

Database: Published Applications AA Main:*

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2	30	100.0	13	4	US-10-705-857-3
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44	27	90.0	240	4	US-10-029-386-33812	Sequence 33812, A
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173	26	86.7	305	4	US-10-128-714-3145	Sequence 3145, Ap	246	26	86.7	1057	4	US-10-425-115-325370	Sequence 325370, A

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OM protein - protein search, using sw model

Run on: February 9, 2006, 13:13:31 / Search time 8 Seconds

(without alignments)
9.842 Million cell updates/sec

Title: US-10-705-857-2

Perfect score: 30

Sequence: 1 BEMORR 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 97014 seqs, 13122538 residues

Total number of hits satisfying chosen parameters: 97014

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 100 summaries

Database : Published Applications AA New:*

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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5	25	83.3	241	7	US-11-152-366-279
6	25	83.3	265	7	US-11-098-686-10694
7	25	83.3	290	6	US-10-467-657-5128
8	25	83.3	323	7	US-11-152-366-38
9	25	83.3	359	7	US-11-129-143-178
10	25	83.3	390	7	US-10-878-556A-162
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12	25	83.3	469	6	US-10-878-556A-101
13	25	83.3	470	6	US-10-878-556A-101
14	25	83.3	558	6	US-10-467-657-4258
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OM protein - protein search, using sw model

Run on: February 9, 2006, 13:25:17, Search time 599 Seconds
(without alignments)
13.843 Million cell updates/sec

Title: us-10-705-857-2

Perfect score: 30
Sequence: 1 BEMQRR 6

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 7861189 seqs, 1381955077 residues

Total number of hits satisfying chosen parameters: 7861189

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Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 1000 summaries

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51: /cgn2_6/ptodata/1/paa/US607_COMB.pep:*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Fri Feb 10 09:12:21 2006

us-10-

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on: February 9, 2006, 13:25:37, Search time 34 Seconds
(without alignments)
12.433 Million cell updates/sec

Title: us-10-705-857-2

Perfect score: 30
Sequence: 1 BEMQRR 6

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 267388 seqs, 70454031 residues

Total number of hits satisfying chosen parameters: 267388

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 1000 summaries

Database:

```

Pending Patents_AA_New:*
1: /cgn2_6/ptodata/2/paa/US067_NEW_COMB.pep:*
2: /cgn2_6/ptodata/2/paa/US067_NEW_COMB.pep:*
3: /cgn2_6/ptodata/2/paa/US073_NEW_COMB.pep:*
4: /cgn2_6/ptodata/2/paa/US073_NEW_COMB.pep:*
5: /cgn2_6/ptodata/2/paa/US075_NEW_COMB.pep:*
6: /cgn2_6/ptodata/2/paa/US075_NEW_COMB.pep:*
7: /cgn2_6/ptodata/2/paa/US077_NEW_COMB.pep:*
8: /cgn2_6/ptodata/2/paa/US078_NEW_COMB.pep:*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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